

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/542,284
Source: PCT
Date Processed by STIC: 07/25/2005

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 07/25/2005

PATENT APPLICATION: US/10/542,284

TIME: 12:01:42

Input Set : A:\AM100238 SEQ Listing.txt

Output Set: N:\CRF4\07252005\J542284.raw

3 <110> APPLICANT: Wyeth Holdings Corporation
 5 <120> TITLE OF INVENTION: METHODS FOR INCREASING NEISSERIA PROTEIN EXPRESSION AND
 6 COMPOSITIONS THEREOF
 8 <130> FILE REFERENCE: AM100238
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/542,284
 C--> 10 <141> CURRENT FILING DATE: 2005-07-15
 10 <160> NUMBER OF SEQ ID NOS: 83
 12 <170> SOFTWARE: PatentIn version 3.2
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 1110
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Neisseria meningitidis (group B)
 19 <400> SEQUENCE: 1

20	atggatgtca	gcctgtacgg	cgaaatcaaa	gccggcgtgg	aaggcaggaa	catccagctg	60
22	cagttgaccg	aaccgctccc	aaatattcaa	cctcagggtta	ctaagcgcaa	aagccgcatac	120
24	aggacgaaaa	tcagcgattt	cggtctgttt	atcggtctta	aggggagtga	ggatttgggc	180
26	gaagggctga	aggctgtttg	gcagcttgag	caagacgtat	ccgttgccgg	cggcggcgcg	240
28	tcccagtggg	gcaacaggga	atcctttatc	ggcttggcag	gcgaattcgg	tacgtgcgc	300
30	gccggtcgcg	ttgcaaatac	gtttgacgat	gccagccaag	ccattgatcc	ttgggacagc	360
32	aataatgatg	tggcttcgca	attgggtatt	ttcaaacgcc	acgacgatat	gtcggtttcc	420
34	gtacgctacg	attcccccca	attttccggt	tttagcggca	gcgtccaatt	cgttccggcc	480
36	caaacagca	agtcgccta	tacgccggct	cattttgttc	agaataagca	aatcagcgg	540
38	cctactctcg	ttccggctgt	tgtcggcaag	ccggggctcg	atgtgtatta	tgccggtctg	600
40	aattacaaaa	atggcggttt	tgccgggaac	tatgccttta	aatacgcgaa	acacgccaat	660
42	gtgggcccgtg	atgcttttga	gttgttcttg	atcggcagcg	cgacgagtga	tgaagccaaa	720
44	ggtaccgatc	ccttgaaaaa	ccatcaggta	caccgcctga	cgggcggcta	tgagggaaggc	780
46	ggcttgaatc	tcgccttggc	ggcccagttg	gatttgtctg	aaaatggcga	caaagccaaa	840
48	acaaaaaaca	gtacgaccga	aattgccgcg	actgcttcc	accgcttcgg	taatgcagtt	900
50	ccacgcatca	gctatgccc	tggtttcgac	ttgatcgaa	gcggtaaaaa	aggcgaaaat	960
52	accagctacg	atcaaatcat	cgccggcggt	gattatgatt	tttccaaacg	cacttccgcc	1020
54	atcgtgtctg	gcgcttggt	gaaacgcaat	accggcatcg	gcaactacac	tcaaattaat	1080
56	gccgcctcgg	tcggtttgcg	ccacaaatc				1110

59 <210> SEQ ID NO: 2
 60 <211> LENGTH: 1057
 61 <212> TYPE: PRT
 62 <213> ORGANISM: Neisseria meningitidis (group B)
 64 <400> SEQUENCE: 2

66	Met	Glu	Thr	Ala	Ser	Pro	Val	Ala	Leu	Ser	Glu	Arg	Leu	Glu	Thr	Tyr
67	1				5					10					15	
70	Arg	Gly	Leu	Tyr	Gly	Leu	Ile	Leu	Glu	Leu	Tyr	Ser	Ala	Leu	Ala	Gly
71			20						25					30		
74	Leu	Tyr	Val	Ala	Leu	Gly	Leu	Gly	Leu	Tyr	Ala	Arg	Gly	Ala	Ser	Asn
75			35						40				45			

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```

78 Ile Leu Glu Gly Leu Asn Leu Glu Gly Leu Asn Leu Glu Thr His Arg
79      50                      55                      60
82 Gly Leu Pro Arg Leu Glu Pro Arg Ala Ser Asn Ile Leu Glu Gly Leu
83 65                      70                      75                      80
86 Asn Pro Arg Gly Leu Asn Val Ala Leu Thr His Arg Leu Tyr Ser Ala
87                      85                      90                      95
90 Arg Gly Leu Tyr Ser Ser Glu Arg Ala Arg Gly Ile Leu Glu Ala Arg
91                      100                      105                      110
94 Gly Thr His Arg Leu Tyr Ser Ile Leu Glu Ser Glu Arg Ala Ser Pro
95                      115                      120                      125
98 Pro His Glu Gly Leu Tyr Ser Glu Arg Pro His Glu Ile Leu Glu Gly
99      130                      135                      140
102 Leu Tyr Pro His Glu Leu Tyr Ser Gly Leu Tyr Ser Glu Arg Gly Leu
103 145                      150                      155                      160
106 Ala Ser Pro Leu Glu Gly Leu Tyr Gly Leu Gly Leu Tyr Leu Glu Leu
107                      165                      170                      175
110 Tyr Ser Ala Leu Ala Val Ala Leu Thr Arg Pro Gly Leu Asn Leu Glu
111                      180                      185                      190
114 Gly Leu Gly Leu Asn Ala Ser Pro Val Ala Leu Ser Glu Arg Val Ala
115                      195                      200                      205
118 Leu Ala Leu Ala Gly Leu Tyr Gly Leu Tyr Gly Leu Tyr Ala Leu Ala
119      210                      215                      220
122 Ser Glu Arg Gly Leu Asn Thr Arg Pro Gly Leu Tyr Ala Ser Asn Ala
123 225                      230                      235                      240
126 Arg Gly Gly Leu Ser Glu Arg Pro His Glu Ile Leu Glu Gly Leu Tyr
127                      245                      250                      255
130 Leu Glu Ala Leu Ala Gly Leu Tyr Gly Leu Pro His Glu Gly Leu Tyr
131                      260                      265                      270
134 Thr His Arg Leu Glu Ala Arg Gly Ala Leu Ala Gly Leu Tyr Ala Arg
135      275                      280                      285
138 Gly Val Ala Leu Ala Leu Ala Ala Ser Asn Gly Leu Asn Pro His Glu
139      290                      295                      300
142 Ala Ser Pro Ala Ser Pro Ala Leu Ala Ser Glu Arg Gly Leu Asn Ala
143 305                      310                      315                      320
146 Leu Ala Ile Leu Glu Ala Ser Pro Pro Arg Thr Arg Pro Ala Ser Pro
147                      325                      330                      335
150 Ser Glu Arg Ala Ser Asn Ala Ser Asn Ala Ser Pro Val Ala Leu Ala
151                      340                      345                      350
154 Leu Ala Ser Glu Arg Gly Leu Asn Leu Glu Gly Leu Tyr Ile Leu Glu
155      355                      360                      365
158 Pro His Glu Leu Tyr Ser Ala Arg Gly His Ile Ser Ala Ser Pro Ala
159      370                      375                      380
162 Ser Pro Met Glu Thr Ser Glu Arg Val Ala Leu Ser Glu Arg Val Ala
163 385                      390                      395                      400
166 Leu Ala Arg Gly Thr Tyr Arg Ala Ser Pro Ser Glu Arg Pro Arg Gly
167                      405                      410                      415
170 Leu Pro His Glu Ser Glu Arg Gly Leu Tyr Pro His Glu Ser Glu Arg
171      420                      425                      430
174 Gly Leu Tyr Ser Glu Arg Val Ala Leu Gly Leu Asn Pro His Glu Val

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```

175          435          440          445
178 Ala Leu Pro Arg Ala Leu Ala Gly Leu Asn Ala Ser Asn Ser Glu Arg
179          450          455          460
182 Leu Tyr Ser Ser Glu Arg Ala Leu Ala Thr Tyr Arg Thr His Arg Pro
183 465          470          475          480
186 Arg Ala Leu Ala His Ile Ser Pro His Glu Val Ala Leu Gly Leu Asn
187          485          490          495
190 Ala Ser Asn Leu Tyr Ser Gly Leu Asn Ala Ser Asn Gly Leu Asn Ala
191          500          505          510
194 Arg Gly Pro Arg Thr His Arg Leu Glu Val Ala Leu Pro Arg Ala Leu
195          515          520          525
198 Ala Val Ala Leu Val Ala Leu Gly Leu Tyr Leu Tyr Ser Pro Arg Gly
199          530          535          540
202 Leu Tyr Ser Glu Arg Ala Ser Pro Val Ala Leu Thr Tyr Arg Thr Tyr
203 545          550          555          560
206 Arg Ala Leu Ala Gly Leu Tyr Leu Glu Ala Ser Asn Thr Tyr Arg Leu
207          565          570          575
210 Tyr Ser Ala Ser Asn Gly Leu Tyr Gly Leu Tyr Pro His Glu Ala Leu
211          580          585          590
214 Ala Gly Leu Tyr Ala Ser Asn Thr Tyr Arg Ala Leu Ala Pro His Glu
215          595          600          605
218 Leu Tyr Ser Thr Tyr Arg Ala Leu Ala Leu Tyr Ser His Ile Ser Ala
219          610          615          620
222 Leu Ala Ala Ser Asn Val Ala Leu Gly Leu Tyr Ala Arg Gly Ala Ser
223 625          630          635          640
226 Pro Ala Leu Ala Pro His Glu Gly Leu Leu Glu Pro His Glu Leu Glu
227          645          650          655
230 Ile Leu Glu Gly Leu Tyr Ser Glu Arg Ala Leu Ala Thr His Arg Ser
231          660          665          670
234 Glu Arg Ala Ser Pro Gly Leu Ala Leu Ala Leu Tyr Ser Gly Leu Tyr
235          675          680          685
238 Thr His Arg Ala Ser Pro Pro Arg Leu Glu Leu Tyr Ser Ala Ser Asn
239          690          695          700
242 His Ile Ser Gly Leu Asn Val Ala Leu His Ile Ser Ala Arg Gly Leu
243 705          710          715          720
246 Glu Thr His Arg Gly Leu Tyr Gly Leu Tyr Thr Tyr Arg Gly Leu Gly
247          725          730          735
250 Leu Gly Leu Tyr Gly Leu Tyr Leu Glu Ala Ser Asn Leu Glu Ala Leu
251          740          745          750
254 Ala Leu Glu Ala Leu Ala Ala Leu Ala Gly Leu Asn Leu Glu Ala Ser
255          755          760          765
258 Pro Leu Glu Ser Glu Arg Gly Leu Ala Ser Asn Gly Leu Tyr Ala Ser
259          770          775          780
262 Pro Leu Tyr Ser Ala Leu Ala Leu Tyr Ser Thr His Arg Leu Tyr Ser
263 785          790          795          800
266 Ala Ser Asn Ser Glu Arg Thr His Arg Thr His Arg Gly Leu Ile Leu
267          805          810          815
270 Glu Ala Leu Ala Ala Leu Ala Thr His Arg Ala Leu Ala Ser Glu Arg
271          820          825          830

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```

274 Thr Tyr Arg Ala Arg Gly Pro His Glu Gly Leu Tyr Ala Ser Asn Ala
275      835      840      845
278 Leu Ala Val Ala Leu Pro Arg Ala Arg Gly Ile Leu Glu Ser Glu Arg
279      850      855      860
282 Thr Tyr Arg Ala Leu Ala His Ile Ser Gly Leu Tyr Pro His Glu Ala
283 865      870      875      880
286 Ser Pro Leu Glu Ile Leu Glu Gly Leu Ala Arg Gly Gly Leu Tyr Leu
287      885      890      895
290 Tyr Ser Leu Tyr Ser Gly Leu Tyr Gly Leu Ala Ser Asn Thr His Arg
291      900      905      910
294 Ser Glu Arg Thr Tyr Arg Ala Ser Pro Gly Leu Asn Ile Leu Glu Ile
295      915      920      925
298 Leu Glu Ala Leu Ala Gly Leu Tyr Val Ala Leu Ala Ser Pro Thr Tyr
299      930      935      940
302 Arg Ala Ser Pro Pro His Glu Ser Glu Arg Leu Tyr Ser Ala Arg Gly
303 945      950      955      960
306 Thr His Arg Ser Glu Arg Ala Leu Ala Ile Leu Glu Val Ala Leu Ser
307      965      970      975
310 Glu Arg Gly Leu Tyr Ala Leu Ala Thr Arg Pro Leu Glu Leu Tyr Ser
311      980      985      990
314 Ala Arg Gly Ala Ser Asn Thr His Arg Gly Leu Tyr Ile Leu Glu Gly
315      995      1000      1005
318 Leu Tyr Ala Ser Asn Thr Tyr Arg Thr His Arg Gly Leu Asn Ile
319      1010      1015      1020
322 Leu Glu Ala Ser Asn Ala Leu Ala Ala Leu Ala Ser Glu Arg Val
323      1025      1030      1035
326 Ala Leu Gly Leu Tyr Leu Glu Ala Arg Gly His Ile Ser Leu Tyr
327      1040      1045      1050
330 Ser Pro His Glu
331      1055
334 <210> SEQ ID NO: 3
335 <211> LENGTH: 1104
336 <212> TYPE: DNA
337 <213> ORGANISM: Neisseria meningitidis (group B)
339 <400> SEQUENCE: 3
340 atggatgtta gctgtacgg cgaaatcaaa gccggcgtgg aaggcaggaa catccagctg      60
342 cagttgaccg aaccgctcca aaatattcaa caacctcagg ttactaagcg caaaagccgc      120
344 atcaggacga aaatcagcga tttcggtctg tttatcggct ttaaggggag cgaggatttg      180
346 ggcgaagggc tgaaggctgt ttggcagctt gagcaagacg tatccgttgc cggcggcggc      240
348 ggcaccggtt ggggcaacag ggaatccttt gtcggcttgg caggtgaatt cggcacgctg      300
350 cgcgcgggcc gcgttgcgaa tcagtttgac gatgccagca aagccattga tccttgggac      360
352 agcaataatg ttgtggcttc gcaattgggt attttcaaac gccacgacga tatgccggtt      420
354 tccgtacgct acgattcccc ggaattttcc ggtttcagcg gcagcgtcca attcgttccg      480
356 gctcaaaaca gcaagtccgc ctatacgccg gctcattttg ttcagcagac tcctcaaagt      540
358 cagcctactc tcgttccggc tgttgcggc aagccggggg cggtatgtga ttatgccggg      600
360 ctgaattaca aaaatggcgg ttttgccggg aactatgcct ttaaatacgc gaaacacgcc      660
362 aatgtgggcc gtgatgcttt tgagttgttc ttgctcggca gcgggagtga tgaagccaaa      720
364 ggtaccgatc ccttgaaaaa ccatcaggta caccgcctga cgggcggcta tgaggaaggc      780
366 ggcttgaatc tcgccttggc ggctcagttg gatttgcctg aaaatgccga caaaaccaa      840

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368 aacagtacga ccgaaattgc cgccactgct tcctaccgct tcggtaatgc agttccacgc      900
370 atcagctatg cccatggttt cgactttatc gaacgcggta aaaaaggcga aaataccagc      960
372 tacgatcaaa tcatcgccgg cgttgattat gatttttcca aacgcacttc cgccatcgctg    1020
374 tctggcgctt ggctgaaacg caataccggc atcggcaact acactcaaat taatgccgcc      1080
376 tccgtcggtt tgcgccacaa attc                                     1104
379 <210> SEQ ID NO: 4
380 <211> LENGTH: 1050
381 <212> TYPE: PRT
382 <213> ORGANISM: Neisseria meningitidis (group B)
384 <400> SEQUENCE: 4
386 Met Glu Thr Ala Ser Pro Val Ala Leu Ser Glu Arg Leu Glu Thr Tyr
387 1          5          10          15
390 Arg Gly Leu Tyr Gly Leu Ile Leu Glu Leu Tyr Ser Ala Leu Ala Gly
391          20          25          30
394 Leu Tyr Val Ala Leu Gly Leu Gly Leu Tyr Ala Arg Gly Ala Ser Asn
395          35          40          45
398 Ile Leu Glu Gly Leu Asn Leu Glu Gly Leu Asn Leu Glu Thr His Arg
399          50          55          60
402 Gly Leu Pro Arg Leu Glu Gly Leu Asn Ala Ser Asn Ile Leu Glu Gly
403 65          70          75          80
406 Leu Asn Gly Leu Asn Pro Arg Gly Leu Asn Val Ala Leu Thr His Arg
407          85          90          95
410 Leu Tyr Ser Ala Arg Gly Leu Tyr Ser Ser Glu Arg Ala Arg Gly Ile
411          100         105         110
414 Leu Glu Ala Arg Gly Thr His Arg Leu Tyr Ser Ile Leu Glu Ser Glu
415          115         120         125
418 Arg Ala Ser Pro Pro His Glu Gly Leu Tyr Ser Glu Arg Pro His Glu
419          130         135         140
422 Ile Leu Glu Gly Leu Tyr Pro His Glu Leu Tyr Ser Gly Leu Tyr Ser
423 145         150         155         160
426 Glu Arg Gly Leu Ala Ser Pro Leu Glu Gly Leu Tyr Gly Leu Gly Leu
427          165         170         175
430 Tyr Leu Glu Leu Tyr Ser Ala Leu Ala Val Ala Leu Thr Arg Pro Gly
431          180         185         190
434 Leu Asn Leu Glu Gly Leu Gly Leu Asn Ala Ser Pro Val Ala Leu Ser
435          195         200         205
438 Glu Arg Val Ala Leu Ala Leu Ala Gly Leu Tyr Gly Leu Tyr Gly Leu
439          210         215         220
442 Tyr Ala Leu Ala Thr His Arg Ala Arg Gly Thr Arg Pro Gly Leu Tyr
443 225         230         235         240
446 Ala Ser Asn Ala Arg Gly Gly Leu Ser Glu Arg Pro His Glu Val Ala
447          245         250         255
450 Leu Gly Leu Tyr Leu Glu Ala Leu Ala Gly Leu Tyr Gly Leu Pro His
451          260         265         270
454 Glu Gly Leu Tyr Thr His Arg Leu Glu Ala Arg Gly Ala Leu Ala Gly
455          275         280         285
458 Leu Tyr Ala Arg Gly Val Ala Leu Ala Leu Ala Ala Ser Asn Gly Leu
459          290         295         300
462 Asn Pro His Glu Ala Ser Pro Ala Ser Pro Ala Leu Ala Ser Glu Arg

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/542,284

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Input Set : A:\AM100238 SEQ Listing.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:26; Xaa Pos. 5
Seq#:27; Xaa Pos. 3
Seq#:29; Xaa Pos. 12
Seq#:30; Xaa Pos. 6
Seq#:31; Xaa Pos. 6
Seq#:32; Xaa Pos. 10
Seq#:81; Xaa Pos. 9,14,22,24,26,30,32,37,38,40,41,42,44,45,47,49,57,58,59
Seq#:81; Xaa Pos. 73,79,80,81,83,87,88,92,98,102,106,107,111,113,114,115
Seq#:81; Xaa Pos. 116,117,118,119,120,121,122,123,124,125,126,128,130,131
Seq#:81; Xaa Pos. 132,133,134,135,140,142,143,146,147,148,150,152,154,157
Seq#:81; Xaa Pos. 161,162,164,166,168,172,173,177,179,185,188,191,194,195
Seq#:81; Xaa Pos. 196,197,199,203,208,210,211,212,214,215,216,220,222,224
Seq#:81; Xaa Pos. 225,226,228,229,233,236,238,240,241,242,243,244,245,247
Seq#:81; Xaa Pos. 249,250,252
Seq#:82; Xaa Pos. 14,22,24,26,30,32,37,38,40,41,42,44,45,47,49,57,58,59,73
Seq#:82; Xaa Pos. 79,80,81,83,88,92,102,146,161,162,164,166,168,172,173,177
Seq#:82; Xaa Pos. 179,194,215,226,236,242,249,252
Seq#:83; Xaa Pos. 9,14,30,32,37,38,40,41,42,44,45,47,49,87,114,117,119,121
Seq#:83; Xaa Pos. 128,130,147,148,149,192,195,196,204,229,230

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:81,82,83

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2544 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:2561 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
L:2589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0
L:2610 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
L:2627 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
L:2644 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
L:3518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81 after pos.:0
M:341 Repeated in SeqNo=81
L:3758 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82 after pos.:0
M:341 Repeated in SeqNo=82
L:3938 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83 after pos.:0
M:341 Repeated in SeqNo=83